

svz
a1

Sequence listing

(1) Name of applicant: JAPAN TABACCO INC.

(2) Title of the invention: Cell Surface Molecule Mediating Cell Adhesion and Signal Transmission

5 (3) Reference number: J1-802PCT

(4) Application number:

(5) Filing date:

(6) Country where the priority application was filed and the application number of the application:

10 Japan, No. Hei 9-062290

Japan, Patent Application filed on February 26, 1998 (reference number, J1-802DP1)

(7) Priority date: February 27, 1997

(8) Number of sequences: 12

15 SEQ ID NO: 1:

SEQUENCE LENGTH: 600

SEQUENCE TYPE: nucleic acid

TOPOLOGY: linear

20 MOLECULE TYPE: cDNA to mRNA

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

25 LOCATION: 1 .. 600

IDENTIFICATION METHOD: E

SEQUENCE DESCRIPTION: SEQ ID NO: 1

ATG AAG TCA GGC CTC TGG TAT TTC TTT CTC 30

Met Lys Ser Gly Leu Trp Tyr Phe Phe Leu

30 1 5 10

TTC TGC TTG CGC ATT AAA GTT TTA ACA GGA 60

Phe Cys Leu Arg Ile Lys Val Leu Thr Gly

15 20

GAA ATC AAT GGT TCT GCC AAT TAT GAG ATG 90

35 Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met

25 30

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	TTT ATA TTT CAC AAC GGA GGT GTA CAA ATT	120
	Phe Ile Phe His Asn Gly Gly Val Gln Ile	
	35 40	
	TTA TGC AAA TAT CCT GAC ATT GTC CAG CAA	150
5	Leu Cys Lys Tyr Pro Asp Ile Val Gln Gln	
	45 50	
	TTT AAA ATG CAG TTG CTG AAA GGG GGG CAA	180
	Phe Lys Met Gln Leu Leu Lys Gly Gly Gln	
	55 60	
10	ATA CTC TGC GAT CTC ACT AAG ACA AAA GGA	210
	Ile Leu Cys Asp Leu Thr Lys Thr Lys Gly	
	65 70	
	AGT GGA AAC ACA GTG TCC ATT AAG AGT CTG	240
	Ser Gly Asn Thr Val Ser Ile Lys Ser Leu	
15	75 80	
	AAA TTC TGC CAT TCT CAG TTA TCC AAC AAC	270
	Lys Phe Cys His Ser Gln Leu Ser Asn Asn	
	85 90	
	AGT GTC TCT TTT TTT CTA TAC AAC TTG GAC	300
20	Ser Val Ser Phe Phe Leu Tyr Asn Leu Asp	
	95 100	
	CAT TCT CAT GCC AAC TAT TAC TTC TGC AAC	330
	His Ser His Ala Asn Tyr Tyr Phe Cys Asn	
	105 110	
25	CTA TCA ATT TTT GAT CCT CCT CCT TTT AAA	360
	Leu Ser Ile Phe Asp Pro Pro Pro Phe Lys	
	115 120	
	GTA ACT CTT ACA GGA GGA TAT TTG CAT ATT	390
	Val Thr Leu Thr Gly Gly Tyr Leu His Ile	
30	125 130	
	TAT GAA TCA CAA CTT TGT TGC CAG CTG AAG	420
	Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys	
	135 140	
	TTC TGG TTA CCC ATA GGA TGT GCA GCC TTT	450
35	Phe Trp Leu Pro Ile Gly Cys Ala Ala Phe	
	145 150	

GTT GTA GTC TGC ATT TTG GGA TGC ATA CTT
Val Val Val Cys Ile Leu Gly Cys Ile Leu
155 160

480

ATT TGT TGG CTT ACA AAA AAG AAG TAT TCA
5 Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser
165 170

510

TCC AGT GTG CAC GAC CCT AAC GGT GAA TAC
Ser Ser Val His Asp Pro Asn Gly Glu Tyr
175 180

540

10 ATG TTC ATG AGA GCA GTG AAC ACA GCC AAA
Met Phe Met Arg Ala Val Asn Thr Ala Lys
185 190

570

AAA TCT AGA CTC ACA GAT GTG ACC CTA TAA
Lys Ser Arg Leu Thr Asp Val Thr Leu
15 195

600

SEQUENCE ID NO: 2:

SEQUENCE LENGTH: 199

SEQUENCE TYPE: amino acid

20 TOPOLOGY: linear

MOLECULE TYPE: protein

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

SEQUENCE DESCRIPTION: SEQ ID NO: 2

25 Met Lys Ser Gly Leu Trp Tyr Phe Phe Leu
1 5 10

Phe Cys Leu Arg Ile Lys Val Leu Thr Gly
15 20

30 Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met
25 30

Phe Ile Phe His Asn Gly Gly Val Gln Ile
35 40

Leu Cys Lys Tyr Pro Asp Ile Val Gln Gln
45 50

35 Phe Lys Met Gln Leu Leu Lys Gly Gly Gln
55 60

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Ile Leu Cys Asp Leu Thr Lys Thr Lys Gly
65 70
Ser Gly Asn Thr Val Ser Ile Lys Ser Leu
75 80
5 Lys Phe Cys His Ser Gln Leu Ser Asn Asn
85 90
Ser Val Ser Phe Phe Leu Tyr Asn Leu Asp
95 100
His Ser His Ala Asn Tyr Tyr Phe Cys Asn
10 105 110
Leu Ser Ile Phe Asp Pro Pro Pro Phe Lys
115 120
Val Thr Leu Thr Gly Gly Tyr Leu His Ile
125 130
15 Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys
135 140
Phe Trp Leu Pro Ile Gly Cys Ala Ala Phe
145 150
Val Val Val Cys Ile Leu Gly Cys Ile Leu
20 155 160
Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser
165 170
Ser Ser Val His Asp Pro Asn Gly Glu Tyr
175 180
25 Met Phe Met Arg Ala Val Asn Thr Ala Lys
185 190
Lys Ser Arg Leu Thr Asp Val Thr Leu
195

30 SEQUENCE ID NO: 3:
SEQUENCE LENGTH: 2610
SEQUENCE TYPE: nucleic acid
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acids (cDNA containing 3'- and 5'-untranslated
35 sequences)
ORIGINAL SOURCE:

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: 26 .. 625

5 IDENTIFICATION METHOD: E

SEQUENCE DESCRIPTION: SEQ ID NO: 3

GGACTGTAA CTGTTTCTGG CAAAC 25

ATG AAG TCA GGC CTC TGG TAT TTC TTT CTC 55

Met Lys Ser Gly Leu Trp Tyr Phe Phe Leu

10 5 10

TTC TGC TTG CGC ATT AAA GTT TTA ACA GGA 85

Phe Cys Leu Arg Ile Lys Val Leu Thr Gly

15 20

GAA ATC AAT GGT TCT GCC AAT TAT GAG ATG 115

15 Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met

25 30

TTT ATA TTT CAC AAC GGA GGT GTA CAA ATT 145

Phe Ile Phe His Asn Gly Gly Val Gln Ile

35 40

20 TTA TGC AAA TAT CCT GAC ATT GTC CAG CAA 175

Leu Cys Lys Tyr Pro Asp Ile Val Gln Gln

45 50

TTT AAA ATG CAG TTG CTG AAA GGG GGG CAA 205

Phe Lys Met Gln Leu Leu Lys Gly Gly Gln

25 55 60

ATA CTC TGC GAT CTC ACT AAG ACA AAA GGA 235

Ile Leu Cys Asp Leu Thr Lys Thr Lys Gly

65 70

AGT GGA AAC ACA GTG TCC ATT AAG AGT CTG 265

30 Ser Gly Asn Thr Val Ser Ile Lys Ser Leu

75 80

AAA TTC TGC CAT TCT CAG TTA TCC AAC AAC 295

Lys Phe Cys His Ser Gln Leu Ser Asn Asn

85 90

35 AGT GTC TCT TTT TTT CTA TAC AAC TTG GAC 325

Ser Val Ser Phe Phe Leu Tyr Asn Leu Asp

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		95	100	
	CAT TCT CAT GCC AAC TAT TAC TTC TGC AAC			355
	His Ser His Ala Asn Tyr Tyr Phe Cys Asn			
		105	110	
5	CTA TCA ATT TTT GAT CCT CCT CCT TTT AAA			385
	Leu Ser Ile Phe Asp Pro Pro Pro Phe Lys			
		115	120	
	GTA ACT CTT ACA GGA GGA TAT TTG CAT ATT			415
	Val Thr Leu Thr Gly Gly Tyr Leu His Ile			
10		125	130	
	TAT GAA TCA CAA CTT TGT TGC CAG CTG AAG			445
	Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys			
		135	140	
	TTC TGG TTA CCC ATA GGA TGT GCA GCC TTT			475
15	Phe Trp Leu Pro Ile Gly Cys Ala Ala Phe			
		145	150	
	GTT GTA GTC TGC ATT TTG GGA TGC ATA CTT			505
	Val Val Val Cys Ile Leu Gly Cys Ile Leu			
		155	160	
20	ATT TGT TGG CTT ACA AAA AAG AAG TAT TCA			535
	Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser			
		165	170	
	TCC AGT GTG CAC GAC CCT AAC GGT GAA TAC			565
	Ser Ser Val His Asp Pro Asn Gly Glu Tyr			
		175	180	
25	ATG TTC ATG AGA GCA GTG AAC ACA GCC AAA			595
	Met Phe Met Arg Ala Val Asn Thr Ala Lys			
		185	190	
	AAA TCT AGA CTC ACA GAT GTG ACC CTA TAA			625
30	Lys Ser Arg Leu Thr Asp Val Thr Leu			
		195		
	TATGGAATC TGGCACCAG GCATGAAGCA CGTTGGCCAG TTTTCCTCAA			675
	CTTGAAGTGC AAGATTCTCT TATTTCCGGG ACCACGGAGA GTCTGACTTA			725
	ACTACATACA TCTTCTGCTG GTGTTTTGTT CAATCTGGAA GAATGACTGT			775
35	ATCAGTCAAT GGGGATTTTA ACAGACTGCC TTGGTACTGC CGAGTCCTCT			825
	CAAAACAAAC ACCCTCTTGC AACCAGCTTT GGAGAAAGCC CAGCTCCTGT			875

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	GTGCTCACTG	GGAGTGGAAT	CCCTGTCTCC	ACATCTGCTC	CTAGCAGTGC	925
	ATCAGCCAGT	AAAACAAACA	CATTTACAAG	AAAAATGTTT	TAAAGATGCC	975
	AGGGGTACTG	AATCTGCAAA	GCAAATGAGC	AGCCAAGGAC	CAGCATCTGT	1025
	CCGCATTTC	CTATCATACT	ACCTCTTCTT	TCTGTAGGGR	TGAGAATTCC	1075
5	TCTTTTAATC	AGTCAAGGGA	GATGCTTCAA	AGCTGGRGCT	ATTTTATTTC	1125
	TGAGATGTTG	ATGTGAACTG	TACATTAGTA	CATACTCAGT	ACTCTCCTTC	1175
	AATTGCTGAA	CCCCAGTTGA	CCATTTTACC	AAGACTTTAG	ATGCTTTCTT	1225
	GTGCCCTCAA	TTTTCTTTTT	AAAAATACTT	CTACATGACT	GCTTGACAGC	1275
	CCAACAGCCA	CTCTCAATAG	AGAGCTATGT	CTTACATTCT	TTCCTCTGCT	1325
10	GCTCAATAGT	TTTATATATC	TATGCATACA	TATATACACA	CATATGTATA	1375
	TAAAATTCAT	AATGAATATA	TTTGCCTATA	TTCTCCCTAC	AAGAATATTT	1425
	TTGCTCCAGA	AAGACATGTT	CTTTTCTCAA	ATTCAGTTAA	AATGGTTTAC	1475
	TTTGTTCAG	TTAGTGGTAG	GAAACATTGC	CCGGAATTGA	AAGCAAATTT	1525
	AWWTTATTAT	CCTATTTTCT	ACCATTATCT	ATGTTTTCAT	GGTGCTATTA	1575
15	ATTACAAGTT	TAGTTCTTTT	TGTAGATCAT	ATTAAAATTG	CAAACAAAAT	1625
	CATCTTTAAT	GGGCCAGCAT	TCTCATGGGG	TAGAGCAGAA	TATTCATTTA	1675
	GCCTGAAAGC	TGCAGTTACT	ATAGGTTGCT	GTCAGACTAT	ACCCATGGTG	1725
	CCTCTGGGCT	TGACAGGTCA	AAATGGTCCC	CATCAGCCTG	GAGCAGCCCT	1775
	CCAGACCTGG	GTGGAATTCC	AGGGTTGAGA	GACTCCCCTG	AGCCAGAGGC	1825
20	CACTAGGTAT	TCTTGCTCCC	AGAGGCTGAA	GTCACCCTGG	GAATCACAGT	1875
	GGTCTACCTG	CATTATAAT	TCCAGGATCT	GTGAAGAGCA	CATATGTGTC	1925
	AGGGCACAAT	TCCCTCTCAT	AAAAAOCACA	CAGCCTGGAA	ATTGGCCCTG	1975
	GCCCTTCAAG	ATAGCCTTCT	TTAGAATATG	ATTTGGCTAG	AAAGATTCTT	2025
	AAATATGTGG	AATATGATTA	TTCTTAGCTG	GAATATTTTC	TCTACTTCCT	2075
25	GTCTGCATGC	CCAAGGCTTC	TGAAGCAGCC	AATGTGCATG	CAACAACATT	2125
	TGTAACTTTA	GGTAAACTGG	GATTATGTTG	TAGTTTAACA	TTTTGTAECT	2175
	GTGTGCTTAT	AGTTTACAAG	TGAGACCCGA	TATGTCATTA	TGCATACTTA	2225
	TATTATCTTA	AGCATGTGTA	ATGCTGGATG	TGTACAGTAC	AGTACWTAAC	2275
	TTGTAATTTG	AATCTAGTAT	GGTGTTCCTG	TTTCAGCTGA	CTTGGACAAC	2325
30	CTGACTGGCT	TTGCACAGGT	GTTCCCTGAG	TTGTTTGCAG	GTTTCTGTGT	2375
	GTGGGGTGGG	GTATGGGGAG	GAGAACCCTC	ATGGTGGCCC	ACCTGGCCTG	2425
	GTTGTCCAAG	CTGTGCCTCG	ACACATCCTC	ATCCCAAGCA	TGGGACACCT	2475
	CAAGATGAAT	AATAATTAC	AAAATTTCTG	TGAAATCAAA	TCCAGTTTTA	2525
	AGAGGAGCCA	CTTATCAAAG	AGATTTTAAC	AGTAGTAAGA	AGGCAAAGAA	2575
35	TAAACATTTG	ATATTCAGCA	ACTGAAAAAA	AAAAA		2610

SEQ ID NO: 4:

SEQUENCE LENGTH: 2072

SEQUENCE TYPE: nucleic acid

TOPOLOGY: linear

5 MOLECULE TYPE: other nucleic acids (cDNA containing 3'- and 5'-untranslated sequences)

ORIGINAL SOURCE:

ORGANISM: Rattus

FEATURE:

10 NAME/KEY: CDS

LOCATION: 35 .. 637

IDENTIFICATION METHOD: E

SEQUENCE DESCRIPTION: SEQ ID NO: 4

CTGGAGGGGA AGAGTGCAGC TGTTCTGGC AGAC 34

15 ATG AAG CCC TAC TTC TCG TGC GTC TTT GTC 64

Met Lys Pro Tyr Phe Ser Cys Val Phe Val

1 5 10

TTC TGC TTC CTA ATC AAA CTT TTA ACA GGA 94

Phe Cys Phe Leu Ile Lys Leu Leu Thr Gly

20 15 20

GAA CTC AAT GAC TTG GCC AAT CAC AGG ATG 124

Glu Leu Asn Asp Leu Ala Asn His Arg Met

25 25 30

TTT TCG TTT CAC GAT GGA GGT GTA CAG ATT 154

25 Phe Ser Phe His Asp Gly Gly Val Gln Ile

35 40

TCT TGT AAC TAC CCT GAG ACT GTC CAG CAG 184

Ser Cys Asn Tyr Pro Glu Thr Val Gln Gln

45 50

30 TTA AAA ATG CAG TTG TTC AAA GAC AGA GAA 214

Leu Lys Met Gln Leu Phe Lys Asp Arg Glu

55 60

GTC CTC TGC GAC CTC ACC AAG ACC AAG GGA 244

Val Leu Cys Asp Leu Thr Lys Thr Lys Gly

35 65 70

AGC GGA AAC ACC GTG TCC ATC AAG AAT CCG 274

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	Ser	Gly	Asn	Thr	Val	Ser	Ile	Lys	Asn	Pro	
					75					80	
	ATG	TCC	TGT	CCA	TAT	CAG	CTG	TCC	AAC	AAC	304
	Met	Ser	Cys	Pro	Tyr	Gln	Leu	Ser	Asn	Asn	
5					85					90	
	AGT	GTC	TCT	TTT	TTC	CTA	GAC	AAC	GCA	GAC	334
	Ser	Val	Ser	Phe	Phe	Leu	Asp	Asn	Ala	Asp	
					95					100	
	AGC	TCC	CAG	GGC	AGC	TAC	TTT	TTA	TGC	AGC	364
10	Ser	Ser	Gln	Gly	Ser	Tyr	Phe	Leu	Cys	Ser	
					105					110	
	CTG	TCG	ATT	TTC	GAC	CCA	CCC	CCT	TTT	CAA	394
	Leu	Ser	Ile	Phe	Asp	Pro	Pro	Pro	Phe	Gln	
					115					120	
15	GAA	AAG	AAC	CTT	AGT	GGA	GGA	TAT	TTG	CTT	424
	Glu	Lys	Asn	Leu	Ser	Gly	Gly	Tyr	Leu	Leu	
					125					130	
	ATT	TAT	GAA	TCC	CAG	CTT	TGT	TGC	CAG	CTG	454
	Ile	Tyr	Glu	Ser	Gln	Leu	Cys	Cys	Gln	Leu	
20					135					140	
	AAG	CTT	TGG	TTA	CCC	GTA	GGG	TGT	GCA	GCT	484
	Lys	Leu	Trp	Leu	Pro	Val	Gly	Cys	Ala	Ala	
					145					150	
	TTT	GTG	GCA	GCG	CTC	CTT	TTT	GGA	TGC	ATA	514
25	Phe	Val	Ala	Ala	Leu	Leu	Phe	Gly	Cys	Ile	
					155					160	
	TTT	ATC	GTC	TGG	TTT	GCA	AAA	AAG	AAG	TAC	544
	Phe	Ile	Val	Trp	Phe	Ala	Lys	Lys	Lys	Tyr	
					165					170	
30	AGA	TCC	AGT	GTG	CAC	GAC	CCT	AAT	AGC	GAG	574
	Arg	Ser	Ser	Val	His	Asp	Pro	Asn	Ser	Glu	
					175					180	
	TAC	ATG	TTC	ATG	GCG	GCA	GTC	AAC	ACA	AAC	604
	Tyr	Met	Phe	Met	Ala	Ala	Val	Asn	Thr	Asn	
35					185					190	
	AAA	AAG	TCC	AGA	CTT	GCA	GGT	ATG	ACC	TCA	634

Lys Lys Ser Arg Leu Ala Gly Met Thr Ser

195

200

TAA 637
TCTGGAACAC GGAACCCAT GGAGGAACTA CACTGTCTAG TTCCCCTGAA 687
5 ACTTGAATGG AGAAAGTCTT CTATTTTCTG GACCACAGGG CATCTGACTT 737
GATTAACCTAC TGATACCTCC TTTTGGKGT TGTGTTGTCT GGATCAGTGA 787
CTATCAGTCA CTCGGAATTT CAGCAGACTG CCCTGGGTTT GCTGAGTCCT 837
TTTAAGGCAA ACCCCTTCTT ATAGAAGACC CGGCTCATAT GTATTCAACA 887
AACAGACCTC ACTGGGATAC AATCCCCCTT TTCTGCGCCT GCTTCTAGCT 937
10 ATGCACCGGC CAGCAAGACA AACATATCTC CAGCATTTTT AAAAAAATGC 987
CAGGGTATGA ATCTGTAAAG TACACAGGCA GCCATTGACC ACCGTCTGTC 1037
CTCGTTTTTT CAGATTCTAT TTTTTTCCAT AGAGATCAGC ATTCCTTCTA 1087
GAATCAGACA GTAGAGGGAG ATGCTTCACA ACAGAAGCTC TTATGTTTCT 1137
GAGATGTTGA TGAATTCATG CTTTAGTACC ACCATGTTCT CTAACAACTT 1187
15 CTATATTCCA GCTGATCACT GCTTCAGGGC TTAGATGCCT GCTTTTGCCT 1237
TCAAGTCTCC CCTTAAAGAT ACTCCACAG GTCTACTTGG TGGCCTGCAG 1287
CCACTCTGAA TAGGAAGTTT GGTCTACAAT TTCCCCCTC TGCTGCTCAA 1337
AAAAAAAAT TAGTAGATAT GATTTTCCCA TATTCTCCCT GCCAAAGTAA 1387
TTTTTTCCAG CAAAGACATC TAAATTCAGT TAATATGGTT TACTGTGTTG 1437
20 ATATTAGTGG CAGTAAACAT TTCTCAGAAT CAAAAGCAAA TTAATTTTGC 1487
GGTGGTGTTC TTCTACCATT ATCTTGGGTT TCCATGGTGC TATTACTCAC 1537
AAGTTTAGCT ATTTTTTTAT GCATCATATT AAAGTTGCAA GCAAGCAGAG 1587
CAACCCTCGG TTAATGGGCA AACATCTCTC TGGGGTAGAA TGAATTGTCT 1637
ATTTAGCCCG AAAACTGCAG TTTCTGTGGG TGGCTGCCAG ACTACAGCCG 1687
25 TGCTTTGCTC TGGCTTTGAC AGGTTGAAAT AGYCCCCATG ASCSTGGAAC 1737
AGWACTCCAG ACTGTGCTGG AGTCCCAAAG TTAGGAGGGC CATGGAGCCT 1787
GGGACAGGCT GCTGCTTTGG TCTTTAGGAT CTAGGAARAA TTACAGAGGG 1837
GCCAAGACAG AGTTCCCTCC CCTAGAAACT GTGCAGCCTG GAAGTCAGCC 1887
CTGGCACTTT AAGATAGCCT TCTTTAGAAC ATGAGTTAGT TGGTAGTATT 1937
30 CTGACGTGTA AACAGCCTAT KGTGCTCGG AGCTGGACCA TTTTCTCCAC 1987
TTCCCTGTCT GCATGCCTAA GACTTCTAGA GCAGCCAACG TATATGCAAC 2037
ATTAAAGAAA AAAAAAAAAA AAAAAAAAAA AAAAA 2072

SEQ ID NO: 5:

35 SEQUENCE LENGTH: 603

SEQUENCE TYPE: nucleic acid

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

ORIGINAL SOURCE:

ORGANISM: Mus

5 FEATURE:

NAME/KEY: CDS

LOCATION: 1 .. 603

IDENTIFICATION METHOD: E

SEQUENCE DESCRIPTION: SEQ ID NO: 5

10 ATG AAG CCG TAC TTC TGC CAT GTC TTT GTC 30
Met Lys Pro Tyr Phe Cys His Val Phe Val
1 5 10
TTC TGC TTC CTA ATC AGA CTT TTA ACA GGA 60
Phe Cys Phe Leu Ile Arg Leu Leu Thr Gly
15 20
GAA ATC AAT GGC TCG GCC GAT CAT AGG ATG 90
Glu Ile Asn Gly Ser Ala Asp His Arg Met
25 30
TTT TCA TTT CAC AAT GGA GGT GTA CAG ATT 120
Phe Ser Phe His Asn Gly Gly Val Gln Ile
35 40
TCT TGT AAA TAC CCT GAG ACT GTC CAG CAG 150
Ser Cys Lys Tyr Pro Glu Thr Val Gln Gln
45 50
25 TTA AAA ATG CGA TTG TTC AGA GAG AGA GAA 180
Leu Lys Met Arg Leu Phe Arg Glu Arg Glu
55 60
GTC CTC TGC GAA CTC ACC AAG ACC AAG GGA 210
Val Leu Cys Glu Leu Thr Lys Thr Lys Gly
30 65 70
AGC GGA AAT GCG GTG TCC ATC AAG AAT CCA 240
Ser Gly Asn Ala Val Ser Ile Lys Asn Pro
75 80
ATG CTC TGT CTA TAT CAT CTG TCA AAC AAC 270
35 Met Leu Cys Leu Tyr His Leu Ser Asn Asn
85 90

SEQUENCE LENGTH: 836

SEQUENCE TYPE: nucleic acid

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acids (cDNA containing 3'- and 5'-untranslated sequences)

ORIGINAL SOURCE:

ORGANISM: Rattus

FEATURE:

NAME/KEY: CDS

LOCATION: 35 .. 685

IDENTIFICATION METHOD: E

SEQUENCE DESCRIPTION: SEQ ID NO: 6

CTGGAGGGGA AGAGTGCAGC TGTTCTTGGC AGAC 34

ATG AAG CCC TAC TTC TCG TGC GTC TTT GTC 64

Met Lys Pro Tyr Phe Ser Cys Val Phe Val

1 5 10

TTC TGC TTC CTA ATC AAA CTT TTA ACA GGA 94

Phe Cys Phe Leu Ile Lys Leu Leu The Gly

15 20

GAA CTC AAT GAC TTG GCC AAT CAC AGG ATG 124

Glu Leu Asn Asp Leu Ala Asn His Arg Met

25 30

TTT TCG TTT CAC GAT GGA GGT GTA CAG ATT 154

Phe Ser Phe His Asp Gly Gly Val Gln Ile

35 40

TCT TGT AAC TAC CCT GAG ACT GTC CAG CAG 184

Ser Cys Asn Tyr Pro Glu Thr Val Gln Gln

45 50

TTA AAA ATG CAG TTG TTC AAA GAC AGA GAA 214

Leu Lys Met Gln Leu Phe Lys Asp Arg Glu

55 60

GTC CTC TGC GAC CTC ACC AAG ACC AAG GGA 244

Val Leu Cys Asp Leu Thr Lys Thr Lys Gly

65 70

AGC GGA AAC ACC GTG TCC ATC AAG AAT CCG 274

Ser Gly Asn Thr Val Ser Ile Lys Asn Pro

					75					80		
		ATG	TCC	TGT	CCA	TAT	CAG	CTG	TCC	AAC	AAC	304
		Met	Ser	Cys	Pro	Tyr	Gln	Leu	Ser	Asn	Asn	
						85					90	
5		AGT	GTC	TCT	TTT	TTC	CTA	GAC	AAC	GCA	GAC	334
		Ser	Val	Ser	Phe	Phe	Leu	Asp	Asn	Ala	Asp	
						95					100	
		AGC	TCC	CAG	GGC	AGC	TAC	TTT	TTA	TGC	AGC	364
		Ser	Ser	Gln	Gly	Ser	Tyr	Phe	Leu	Cys	Ser	
10						105					110	
		CTG	TCG	ATT	TTC	GAC	CCA	CCC	CCT	TTT	CAA	394
		Leu	Ser	Ile	Phe	Asp	Pro	Pro	Pro	Phe	Gln	
						115					120	
		GAA	AAG	AAC	CTT	AGT	GGA	GGA	TAT	TTG	CTT	424
15		Glu	Lys	Asn	Leu	Ser	Gly	Gly	Tyr	Leu	Leu	
						125					130	
		ATT	TAT	GAA	TCC	CAG	CTT	TGT	TGC	CAG	CTG	454
		Ile	Tyr	Glu	Ser	Gln	Leu	Cys	Cys	Gln	Leu	
						135					140	
20		AAG	CTT	TGG	TTA	CCC	GTA	GGG	TGT	GCA	GCT	484
		Lys	Leu	Trp	Leu	Pro	Val	Gly	Cys	Ala	Ala	
						145					150	
		TTT	GTG	GCA	GCG	CTC	CTT	TTT	GGA	TGC	ATA	514
		Phe	Val	Ala	Ala	Leu	Leu	Phe	Gly	Cys	Ile	
25						155					160	
		TTT	ATC	GTC	TGG	TTT	GCA	AAA	AAG	AAG	TAC	544
		Phe	Ile	Val	Trp	Phe	Ala	Lys	Lys	Lys	Tyr	
						165					170	
		AGA	TCC	AGT	GTG	CAC	GAC	CCT	AAT	AGC	GAG	574
30		Arg	Ser	Ser	Val	His	Asp	Pro	Asn	Ser	Glu	
						175					180	
		TAC	ATG	TTC	ATG	GCG	GCA	GTC	AAC	ACA	AAC	604
		Tyr	Met	Phe	Met	Ala	Ala	Val	Asn	Thr	Asn	
						185					190	
35		AAA	AAG	TCC	AGA	CTT	GCA	GGT	ACA	GCA	COC	634
		Lys	Lys	Ser	Arg	Leu	Ala	Gly	Thr	Ala	Pro	

195 200
CTT AGG GCT TTG GGG AGA GGA GAA CAC TCT 664
Leu Arg Ala Leu Gly Arg Gly Glu His Ser

205 210

5 TCA TGT CAA GAC CGG AAT TAA 685
Ser Cys Gln Asp Arg Asn

215

TTTGTTTATT TCTATTTTAA AAGAAAGACA TTTTTCCTCC TAAAGATAAT 735

TTTTGTATTT TTATGTGAAA GTCTGAATCT TCATTTTAAC TCGACTTATA 785

10 TACTCTGTGG TATATTAAAA ATAATGTTTG TGAAAAAAAA AAAAAAAAAA 835

A 836

SEQ ID NO: 7:

SEQUENCE LENGTH: 27

SEQUENCE TYPE: nucleic acid

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acids (synthetic DNA)

FEATURE:

NAME/KEY: primer bind

LOCATION: 1 .. 27

IDENTIFICATION METHOD: E

SEQUENCE DESCRIPTION: SEQ ID NO: 7

CTGCTCGAGA TGAAGCCCTA CTTCTCG 27

SEQ ID NO: 8:

SEQUENCE LENGTH: 32

SEQUENCE TYPE: nucleic acid

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acids (synthetic DNA)

FEATURE:

NAME/KEY: primer bind

LOCATION: 1 .. 32

IDENTIFICATION METHOD: E

SEQUENCE DESCRIPTION: SEQ ID NO: 8

ACCCTACGGG TAACGGATCC TTCAGCTGGC AA 32

SEQ ID NO: 9:

SEQUENCE LENGTH: 30

SEQUENCE TYPE: nucleic acid

TOPOLOGY: linear

5 MOLECULE TYPE: other nucleic acid (synthetic DNA)

FEATURE:

NAME/KEY: primer bind

LOCATION: 1 .. 30

IDENTIFICATION METHOD: E

10 SEQUENCE DESCRIPTION: SEQ ID NO: 9

TAACTGTTTC TCGAGAACAT GAAGTCAGGC

30

SEQ ID NO: 10:

SEQUENCE LENGTH: 30

15 SEQUENCE TYPE: nucleic acid

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid (synthetic DNA)

FEATURE:

NAME/KEY: primer bind

20 LOCATION: 1 .. 30

IDENTIFICATION METHOD: E

SEQUENCE DESCRIPTION: SEQ ID NO: 10

ATCCTATGGG TAACGGATCC TTCAGCTGGC

30

25 SEQ ID NO: 11:

SEQUENCE LENGTH: 35

SEQUENCE TYPE: nucleic acid

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid (synthetic DNA)

30 FEATURE:

NAME/KEY: primer bind

LOCATION: 1 .. 35

IDENTIFICATION METHOD: E

SEQUENCE DESCRIPTION: SEQ ID NO: 11

35 CGTGATATTG CTGAAGAGCT TGGCGGCGAA TGGGC

35

SEQ ID NO: 12:

SEQUENCE LENGTH: 34

SEQUENCE TYPE: nucleic acid

TOPOLOGY: linear

5 MOLECULE TYPE: other nucleic acid (synthetic DNA)

FEATURE:

NAME/KEY: primer bind

LOCATION: 1 .. 34

IDENTIFICATION METHOD: E

10 SEQUENCE DESCRIPTION: SEQ ID NO: 12

CATTCAAGTT TCAGGGAAGT AGTCCATGCG TTTC

34

669280" TGGGEEED